

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: CHARETTE, MARC F.  
RUEGER, DAVID C.  
HIGGINS, DENNIS
- (ii) TITLE OF INVENTION: ENHANCEMENT OF MORPHOGEN ACTIVITY
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
THIBEAULT, LLP  
(B) STREET: 125 HIGH STREET  
(C) CITY: BOSTON  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: MEYERS, THOMAS C.  
(B) REGISTRATION NUMBER: 36,989  
(C) REFERENCE/DOCKET NUMBER: CRP-158PR
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 248-7000  
(B) TELEFAX: (617) 248-7100

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: HOMO SAPIENS  
(F) TISSUE TYPE: HIPPOCAMPUS
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 49..1341  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"  
/product= "OP1"  
/evidence= EXPERIMENTAL  
/standard\_name= "OP1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGTGC GGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
                                     Met His Val
                                     1

CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
Arg Ser 5 Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
                                     10                                     15

CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
20                                     25                                     30                                     35

GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201

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00509649-100500

Glu	Val	His	Ser	Ser 40	Phe	Ile	His	Arg	Arg 45	Leu	Arg	Ser	Gln	Glu 50	Arg	
CGG Arg	GAG Glu	ATG Met	CAG Gln 55	CGC Arg	GAG Glu	ATC Ile	CTC Leu	TCC Ser 60	ATT Ile	TTG Leu	GGC Gly	TTG Leu	CCC Pro 65	CAC His	CGC Arg	249
CCG Pro	CGC Arg	CCG Pro 70	CAC His	CTC Leu	CAG Gln	GGC Gly	AAG Lys 75	CAC His	AAC Asn	TCG Ser	GCA Ala	CCC Pro 80	ATG Met	TTC Phe	ATG Met	297
CTG Leu	GAC Asp 85	CTG Leu	TAC Tyr	AAC Asn	GCC Ala	ATG Met 90	GCG Ala	GTG Val	GAG Glu	GAG Glu	GGC Gly 95	GGC Gly	GGG Gly	CCC Pro	GGC Gly	345
GGC Gly 100	CAG Gln	GGC Gly	TTC Phe	TCC Ser	TAC Tyr 105	CCC Pro	TAC Tyr	AAG Lys	GCC Ala	GTC Val 110	TTC Phe	AGT Ser	ACC Thr	CAG Gln	GGC Gly 115	393
CCC Pro	CCT Pro	CTG Leu	GCC Ala	AGC Ser 120	CTG Leu	CAA Gln	GAT Asp	AGC Ser	CAT His 125	TTC Phe	CTC Leu	ACC Thr	GAC Asp	GCC Ala 130	GAC Asp	441
ATG Met	GTC Val	ATG Met	AGC Ser 135	TTC Phe	GTC Val	AAC Asn	CTC Leu	GTG Val 140	GAA Glu	CAT His	GAC Asp	AAG Lys	GAA Glu 145	TTC Phe	TTC Phe	489
CAC His	CCA Pro	CGC Arg 150	TAC Tyr	CAC His	CAT His	CGA Arg	GAG Glu 155	TTC Phe	CGG Arg	TTT Phe	GAT Asp	CTT Leu 160	TCC Ser	AAG Lys	ATC Ile	537
CCA Pro	GAA Glu 165	GGG Gly	GAA Glu	GCT Ala	GTC Val	ACG Thr 170	GCA Ala	GCC Ala	GAA Glu	TTC Phe	CGG Arg 175	ATC Ile	TAC Tyr	AAG Lys	GAC Asp	585
TAC Tyr 180	ATC Ile	CGG Arg	GAA Glu	CGC Arg	TTC Phe 185	GAC Asp	AAT Asn	GAG Glu	ACG Thr	TTC Phe 190	CGG Arg	ATC Ile	AGC Ser	GTT Val	TAT Tyr 195	633
CAG Gln	GTG Val	CTC Leu	CAG Gln	GAG Glu 200	CAC His	TTG Leu	GGC Gly	AGG Arg	GAA Glu 205	TCG Ser	GAT Asp	CTC Leu	TTC Phe	CTG Leu 210	CTC Leu	681
GAC Asp	AGC Ser	CGT Arg	ACC Thr 215	CTC Leu	TGG Trp	GCC Ala	TCG Ser	GAG Glu 220	GAG Glu	GGC Gly	TGG Trp	CTG Leu	GTG Val 225	TTT Phe	GAC Asp	729
ATC Ile	ACA Thr 230	GCC Ala	ACC Thr	AGC Ser	AAC Asn	CAC His	TGG Trp 235	GTG Val	GTC Val	AAT Asn	CCG Pro	CGG Arg 240	CAC His	AAC Asn	CTG Leu	777
GGC Gly 245	CTG Leu	CAG Gln	CTC Leu	TCG Ser	GTG Val	GAG Glu 250	ACG Thr	CTG Leu	GAT Asp	GGG Gly	CAG Gln 255	AGC Ser	ATC Ile	AAC Asn	CCC Pro	825
AAG Lys 260	TTG Leu	GCG Ala	GGC Gly	CTG Leu	ATT Ile 265	GGG Gly	CGG Arg	CAC His	GGG Gly	CCC Pro 270	CAG Gln	AAC Asn	AAG Lys	CAG Gln	CCC Pro 275	873
TTC Phe	ATG Met	GTG Val	GCT Ala	TTC Phe 280	TTC Phe	AAG Lys	GCC Ala	ACG Thr	GAG Glu 285	GTC Val	CAC His	TTC Phe	CGC Arg	AGC Ser 290	ATC Ile	921
CGG Arg	TCC Ser	ACG Thr 295	GGG Gly	AGC Ser	AAA Lys	CAG Gln	CGC Arg	AGC Ser 300	CAG Gln	AAC Asn	CGC Arg	TCC Ser 305	AAG Lys	ACG Thr	CCC Pro	969
AAG Lys	AAC Asn	CAG Gln 310	GAA Glu	GCC Ala	CTG Leu	CGG Arg	ATG Met 315	GCC Ala	AAC Asn	GTG Val	GCA Ala	GAG Glu 320	AAC Asn	AGC Ser	AGC Ser	1017
AGC Ser	GAC Asp 325	CAG Gln	AGG Arg	CAG Gln	GCC Ala	TGT Cys 330	AAG Lys	AAG Lys	CAC His	GAG Glu	CTG Leu 335	TAT Tyr	GTC Val	AGC Ser	TTC Phe	1065
CGA Arg 340	GAC Asp	CTG Leu	GGC Gly	TGG Trp	CAG Gln 345	GAC Asp	TGG Trp	ATC Ile	ATC Ile	GCG Ala 350	CCT Pro	GAA Glu	GGC Gly	TAC Tyr	GCC Ala 355	1113
GCC Ala	TAC Tyr	TAC Tyr	TGT Cys	GAG Glu	GGG Gly	GAG Glu	TGT Cys	GCC Ala	TTC Phe	CCT Pro	CTG Leu	AAC Asn	TCC Ser	TAC Tyr	ATG Met	1161

360	365	370	
AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385			1209
CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400			1257
ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415			1305
TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430			1351
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGCCAG			1411
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG			1471
TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC			1531
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC			1591
GCATAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT			1651
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG			1711
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC			1771
CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A			1822

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala  
1 5 10 15  
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser  
20 25 30  
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
35 40 45  
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
50 55 60  
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
65 70 75 80  
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
85 90 95  
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
100 105 110  
Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
115 120 125  
Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
130 135 140  
Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
145 150 155 160  
Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
165 170 175  
Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
 195 200 205  
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
 210 215 220  
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
 225 230 235 240  
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
 245 250 255  
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
 260 265 270  
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe  
 275 280 285  
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser  
 290 295 300  
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu  
 305 310 315 320  
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr  
 325 330 335  
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu  
 340 345 350  
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn  
 355 360 365  
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His  
 370 375 380  
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln  
 385 390 395 400  
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
 405 410 415  
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa  
 1 5 10  
 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly  
 20 25 30  
 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala  
 35 40 45  
 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys  
 50 55 60  
 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa

05509643 1.00500

(2) INFORMATION FOR SEQ ID NO:4:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa  
1 5 10 15  
Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly  
20 25 30  
Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 50 55 60  
 Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val  
 85 90 95  
 Xaa Xaa Cys Xaa Cys Xaa  
 100

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME/KEY: Protein  
 (B) LOCATION: 1..97  
 (D) OTHER INFORMATION: /label= Generic-Seq-9  
 /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Pro  
 50 55 60  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys  
 85 90 95  
 Xaa

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME/KEY: Protein  
 (B) LOCATION: 1..102  
 (D) OTHER INFORMATION: /label= Generic-Seq-10  
 /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15

050648 10500

(2) INFORMATION FOR SEQ ID NO:8:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(2) INFORMATION FOR SEQ ID NO:9:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Xaa Xaa Xaa Xaa  
1 5